

☐ 1: AI360308. qy85c09.x1 NCI CG...[gi:4111929]

Links

## IDENTIFIERS

dbEST Id: EST name:

2144126 qy85c09.x1

GenBank Acc: GenBank gi:

AI360308 4111929

CLONE INFO

Clone Id:

IMAGE:2018800 (3')

Source: Insert length:

NCI 553 **CDNA** 

DNA type:

PRIMERS

Sequencing:

-40UP from Gibco

Unknown PolyA Tail:

SEQUENCE

AAGAGAATCATACAGTGGCTTTATTCTTACTACTTAAAAAAAGGTGATGTGATGGCAGTG ATGGTCAACATCACAGGGAAGACCAGGTCCACGCTTTGTCCAGAATCAACTGCTACCA CATGAGTCTTCTTGGTTAAGTCATTTGAGCCCACAGTGACAGAATAGGTCCCTGGATATA CTTCTATGTAGAGGTCCTTAGAGATGTTCTCAGCAGGCTGGGATGCCTCTGGAGCATGCT CTGATATTTGATAGCTGCCTCCAGGACCAAGGGATGTCTTTTTTCTGTCTTTTCTCTGAC CATTCCCTATGTCCAAGCACATGTGCAGCTTCGACTCGCCTCTGTGATAACGATAGACAT GGGTTGCCCCTCCTTCCTCTGGCACAGATGAATAATATTTCCCACACTGACTTGAAGTAT

AGTCCATGAATTCAGCCATTGTTCTGA

Quality: High quality sequence stops at base: 432

Entry Created: Jan 6 1999 Last Updated: Feb 16 1999

COMMENTS

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld

M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing

Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

LIBRARY

Lib Name: Organism: NCI\_CGAP\_Brn25 Homo sapiens

Organ: brain

Tissue type: anaplastic oligodendroglioma

Lab host:

pT7T3D-Pac (Pharmacia) with a modified polylinker Vector:

R. Site 1: Not I R. Site 2: Eco RI

Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

SUBMITTER

Name: E-mail: Robert Strausberg, Ph.D. cgapbs-r@mail.nih.gov

CITATIONS

Title:

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome

Anatomy Project (CGAP/BTGAP), Tumor Gene Index NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap

Authors:

1998

Year: Status:

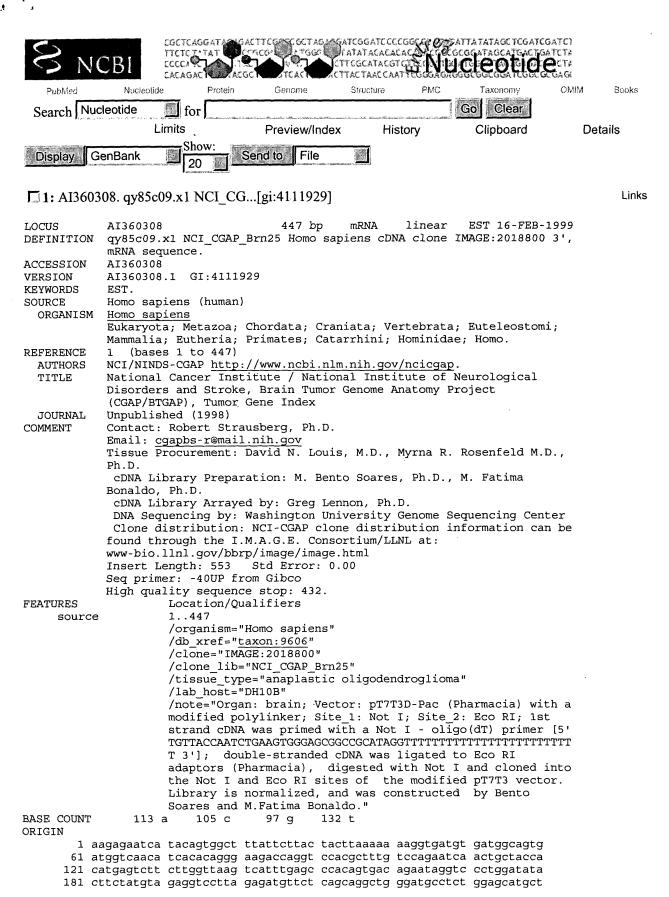
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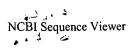
MAP DATA

Revised: July 5, 2002.

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Feb 19 2003 14:49:48





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241 ctgatatttg atagctgcct ccaggaccaa gggatgtctt ttttctgtct tttctctgac 301 cattccctat gtccaagcac atgtgcagct tcgactcgcc tctgtgataa cgatagacat 361 gggttgcccc tccttcctct ggcacagatg aataatattt cccacactga cttgaagtat 421 agtccatgaa ttcagccatt gttctga
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